WHAT IS CLAIMED IS:

1. A solution comprising a molecule or molecular complex that comprises a Bcl-w active site defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Arg59, Asp63, Leu64, Gln67, Phe79, Val82, Val102 and Leu106 as set forth in TABLE 1, or a variant of the molecule or molecular complex, wherein the variant comprises an active site that has a root mean square deviation from the Cα atoms of the amino acid residues defining the Bcl–w active site of not more than 1.1 Å.

2. A solution according to claim 1, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

3. A solution according to claim 1, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

4. A solution according to claim 1, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

5. A solution according to claim 1, wherein the molecule or molecular complex further comprises the C-terminal region of Bcl–w.

6. A solution according to claim 5, wherein the molecule or molecular complex comprises the C-terminal helix (α9, residues 157-173) and extended region (residues 174-183) of Bcl–w.

7. A solution according to claim 1, wherein the molecule or molecular complex comprises a polypeptide that is distinguished from Bcl–w by the deletion of at least one amino acid residue at the C-terminus of Bcl-w.

8. A solution according to claim 7, wherein the polypeptide is further distinguished from Bcl-w by the substitution of at least one hydrophobic amino acid residue with a charged amino acid residue.

9. A solution according to claim 8, wherein the hydrophobic amino acid residue is Ala128 and the charged amino acid residue is glutamate or modified form thereof.

10. A solution according to claim 7, wherein the polypeptide is a Bcl–w derivative that lacks the last 10 amino acid residues of Bcl–w and that has Ala128 substituted with a glutamate residue or modified form thereof.

11. A solution according to claim 7, wherein the polypeptide comprises the sequence set forth in SEQ ID NO:2.

12. A polypeptide that is distinguished from Bcl–w by the deletion of at least one amino acid residue from the C-terminus of Bcl-w.

13. A polypeptide according to claim 12, which is further distinguished from Bcl-w by the substitution of at least one hydrophobic amino acid residue with a charged amino acid residue.

14. A polypeptide according to claim 13, wherein the hydrophobic amino acid residue is Ala128 and the charged amino acid residue is glutamate or modified form thereof.

15. A polypeptide according to claim 12, which is a Bcl–w derivative that lacks the last 10 amino acid residues of Bcl–w and that has Ala128 substituted with a glutamate residue or modified form thereof.

16. A polypeptide according to claim 12, which consists essentially of the sequence set forth in SEQ ID NO:2.

17. A polynucleotide comprising a sequence that encodes a polypeptide that is distinguished from Bcl–w by the deletion of at least one amino acid residue from the C-terminus of Bcl-w.

18. A polynucleotide according to claim 17, wherein the polypeptide is distinguished from Bcl–w by the substitution of at least one hydrophobic amino acid residue with a charged amino acid residue.

19. A vector comprising the polynucleotide of claim 17 or claim 18.

20. A host cell containing the polynucleotide of claim 17 or claim 18.

21. A host cell containing a vector comprising the polynucleotide of claim 17 or claim 18.

22. A data store comprising data representing the structure coordinates of Bcl–w amino acid residues and which are capable of being used by a computer system to generate a three-dimensional representation of a molecule or molecular complex comprising a Bcl–w active site defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Arg59, Asp63, Leu64, Gln67, Phe79, Val82, Val102 and Leu106 as set forth in TABLE 1, or a variant of the molecule or molecular complex, wherein the variant comprises an active site that has a root mean square deviation from the Cα atoms of the amino acid residues defining the Bcl–w active site of not more than 1.1 Å.

23. A data store according to claim 22, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

24. A data store according to claim 22, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

25. A data store according to claim 22, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

26. A computer system having data representing structural coordinates of Bcl–w amino acid residues, the computer system being adapted to generate, on the basis of the data, a three-dimensional representation of a molecule or molecular complex comprising a Bcl–w active site that is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1, or a variant of the molecule or molecular complex, wherein the variant comprises an active site that has a root mean square deviation from the Cα atoms of the amino acid residues defining the Bcl–w active site of not more than 1.1 Å.

27. A computer system according to claim 26, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

28. A computer system according to claim 26, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

29. A computer system according to claim 26, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56,

Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

30. A computer system for producing a three-dimensional representation of a molecule or molecular complex, the computer system comprising:

(a) a data store including data representing the structure coordinates of Bcl–w amino acid residues defining a Bcl–w active site that is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1, or structural coordinates having a root mean square deviation from the Cα atoms of those residues of not more than 1.1 Å;

(b) a processing means for processing the data to generate a three-dimensional representation of a molecule or molecular complex comprising the Bcl–w active site or similarly shaped homologous active site for display; and

(c) a display means for displaying the three-dimensional representation.

31. A computer system according to claim 31, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

32. A computer system according to claim 31, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

33. A computer system according to claim 31, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

34. An analysis method, executed by a computer system, for evaluating the ability of a chemical entity to associate with a molecule or molecular complex comprising an active site, the method comprising the steps of:

(a) generating a model of the active site using structure coordinates wherein the root mean square deviation between the structure coordinates and the structure coordinates of the Bcl–w amino acid residues defining a Bcl–w active site is not more than about 1.1 Å, wherein the Bcl-w active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1;

(b) performing a fitting operation between the chemical entity and the model of the active site; and

(c) quantifying the association between the chemical entity and the active site model, based on the output of the fitting operation.

35. An analysis method according to claim 34, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

36. An analysis method according to claim 34, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

37. An analysis method according to claim 34, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

38. An analysis method, executed by a computer system, for comparing the ability of a chemical entity to associate with a first molecule or molecular complex comprising a first active site and the ability of the chemical entity to associate with a second molecule or molecular complex comprising a second active site, the method comprising the steps of:

(a) generating a model of the first active site using structure coordinates wherein the root mean square deviation between the structure coordinates and the structure coordinates of the Bcl–w amino acid residues defining a Bcl–w active site is not more than about 1.1 Å, wherein the Bcl-w active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1;

(b) performing a first fitting operation between the chemical entity and the model of the first active site;

(c) quantifying the association between the chemical entity and the first active site model, based on the output of the first fitting operation;

(d) performing a second fitting operation between the chemical entity and a model of the second active site;

(e) quantifying the association between the chemical entity and the second active site model, based on the output of the second fitting operation; and

(f) comparing the respective associations of the chemical entity with the first active site model and with the second active site model.

39. An analysis method according to claim 38, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

40. An analysis method according to claim 38, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

41. An analysis method according to claim 38, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

42. An analysis method according to claim 38, wherein the second molecule or molecular complex comprises an active site of another pro-survival protein.

43. An analysis method according to claim 42, wherein the other pro-survival protein is selected from Bcl-2, Bcl-x_L, Mcl-1 and A1, or variant thereof.

44. An analysis method, executed by a computer system, for identifying a chemical entity that associates with both a first molecule or molecular complex comprising a first active site and a second molecule or molecular complex comprising a second active site, the method comprising the steps of:

(a) generating a model of the first active site using structure coordinates wherein the root mean square deviation between the structure coordinates and the structure coordinates of the

Bcl–w amino acid residues defining a Bcl–w active site is not more than about 1.1 Å, wherein the Bcl-w active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1;

(b) performing a fitting operation between the chemical entity and the model of the first active site;

(c) quantifying the association between the chemical entity and the first active site model, based on the output of the first fitting operation;

(d) performing a second fitting operation between the chemical entity and a model of the second active site;

(e) quantifying the association between the chemical entity and the second active site model, based on the output of the second fitting operation; and

(f) comparing the respective associations of the chemical entity with the first active site model and with the second active site model to determine whether the chemical entity associates individually with both the first molecule or molecular complex and the second molecule or molecular complex.

45. An analysis method, executed by a computer system, for identifying a chemical entity that associates more favourably with a first molecule or molecular complex comprising a first active site than with a second molecule or molecular complex comprising a second active site, the method comprising the steps of:

(a) generating a model of the first active site using structure coordinates wherein the root mean square deviation between the structure coordinates and the structure coordinates of the Bcl–w amino acid residues defining a Bcl–w active site is not more than about 1.1 Å, wherein the Bcl-w active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113, as set forth in TABLE 1;

(b) performing a fitting operation between the chemical entity and the model of the first active site;

(c) quantifying the association between the chemical entity and the first active site model, based on the output of the first fitting operation;

(d) performing a second fitting operation between the chemical entity and a model of the second active site;

(e) quantifying the association between the chemical entity and the second active site model, based on the output of the second fitting operation; and

(f) comparing the respective associations of the chemical entity with the first active site model and with the second active site model to determine whether the chemical entity

associates more favourably with the first molecule or molecular complex than with the second molecule or molecular complex.

46. An analysis method according to claim 44 or claim 45, wherein the active site is further defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Glu85, Arg95 and Lys113 as set forth in TABLE 1.

47. An analysis method according to claim 44 or claim 45, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

48. An analysis method according to claim 44 or claim 45, wherein the active site is defined by the structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

49. A method for identifying a potential antagonist of a molecule comprising a Bcl-w-like active site, comprising the steps of:

(a) generating a three-dimensional structure of the molecule comprising the active site using the atomic coordinates of at least three Bcl–w amino acid residues selected from Arg59, Asp63, Leu64, Gln67, Phe79, Val82, Val102 and Leu106 as set forth in TABLE 1 ± a root mean square deviation from the Cα atoms of those residues of not more than 1.1 Å;

(b) employing the three-dimensional structure to identify, design or select the potential antagonist;

(c) synthesising or otherwise obtaining the antagonist; and

(d) contacting the antagonist with the molecule to determine the ability of the potential antagonist to interact with said molecule.

50. A method according to claim 49, wherein the three-dimensional structure of the molecule comprising the active site is generated further using structure coordinates of at least three Bcl–w amino acid residues selected from Glu52, Arg56, Arg58, Asp63, Glu85, Arg95 and Lys113 as set forth in TABLE 1 ± a root mean square deviation from the Cα atoms of those residues of not more than 1.1 Å.

51. A method according to claim 49, wherein the three-dimensional structure of the molecule comprising the active site is generated further using structure coordinates of at least

three Bcl–w amino acid residues selected from Gln44, Ala45, Ala48, Ala49, Gly50, Glu52, Phe53, Arg56, Phe57, Arg58, Arg59, Asp63, Leu64, Ala66, Gln67, His69, Val70, Arg78, Phe79, Gln81, Val82, Ser83, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Val97, Phe99, Phe102, Leu106, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

52. A method according to claim 49, wherein the three-dimensional structure of the molecule comprising the active site is generated further using structure coordinates of at least three Bcl–w amino acid residues selected from Gln44, Ala45, Met46, Arg47, Ala48, Ala49, Gly50, Asp51, Glu52, Phe53, Glu54, Thr55, Arg56, Phe57, Arg58, Arg59, Thr60, Ser62, Asp63, Leu64, Ala65, Ala66, Gln67, Leu68, His69, Val70, Thr71, Ala75, Gln76, Gln77, Arg78, Phe79, Thr80, Gln81, Val82, Ser83, Asp84, Glu85, Leu86, Phe87, Gln88, Gly89, Gly90, Pro91, Asn92, Trp93, Gly94, Arg95, Leu96, Val97, Ala98, Phe99, Phe102, Gly103, Leu106, Trp137, Ser141, Glu146, Phe147, Thr148, Ala149, Leu150, Tyr151 and Gly152, as set forth in TABLE 1.

53. A method according to claim 49, wherein the three-dimensional structure of the molecule comprising the active site is created using the structure coordinates of all the Bcl–w amino acid residues as set forth in TABLE 1 ± a root mean square deviation from the Cα atoms of those residues of not more than 1.1 Å.

54. An agent or antagonist designed or selected using a method according to any one of claims 34 to 53.

55. A method for determining at least a portion of the three-dimensional structure of a molecule or molecular complex which contains at least some features that are structurally similar to Bcl–w by using at least some of the structural coordinates obtained for Bcl–w, the method comprising the steps of:

(a) obtaining crystals or a solution of the molecule or molecular complex whose structure is unknown;

(b) generating X-ray diffraction data from the crystallised molecule or molecular complex and/or generating NMR data from the solution of the molecule or molecular complex;

(c) comparing the data so generated with the solution coordinates or three dimensional structure of a Bcl–w derivative as set forth in TABLE 1, and

(d) modeling the three dimensional structure of the unknown molecule or molecular complex on the basis of the Bcl–w derivative structure.